```
                                        30
    *     *     *     *     *     *     *     *     *
ATG GTG ACA GGC TGG CAT CGT CCA ACA TGG ATT GAA ATA GAC CGC GCA
Met Val Thr Gly Trp His Arg Pro Thr Trp Ile Glu Ile Asp Arg Ala

            60                                          90
 *     *     *     *     *     *     *     *     *     *
GCA ATT CGC GAA AAT ATA AAA AAT GAA CAA AAT AAA CTC CCG GAA AGT
Ala Ile Arg Glu Asn Ile Lys Asn Glu Gln Asn Lys Leu Pro Glu Ser

                        120
    *     *     *     *     *     *     *     *     *
GTC GAC TTA TGG GCA GTA GTC AAA GCT AAT GCA TAT GGT CAC GGA ATT
Val Asp Leu Trp Ala Val Val Lys Ala Asn Ala Tyr Gly His Gly Ile

    150                                         180
 *     *     *     *     *     *     *     *     *     *
ATC GAA GTT GCT AGG ACG GCG AAA GAA GCT GGA GCA AAA GGT TTC TGC
Ile Glu Val Ala Arg Thr Ala Lys Glu Ala Gly Ala Lys Gly Phe Cys

                    210                                 240
   *     *     *     *     *     *     *     *     *     *
GTA GCC ATT TTA GAT GAG GCA CTG GCT CTT AGA GAA GCT GGA TTT CAA
Val Ala Ile Leu Asp Glu Ala Leu Ala Leu Arg Glu Ala Gly Phe Gln

                                    270
    *     *     *     *     *     *     *     *     *
GAT GAC TTT ATT CTT GTG CTT GGT GCA ACC AGA AAA GAA GAT GCT AAT
Asp Asp Phe Ile Leu Val Leu Gly Ala Thr Arg Lys Glu Asp Ala Asn

            300                                         330
 *     *     *     *     *     *     *     *     *     *
CTG GCA GCC AAA AAC CAC ATT TCA CTT ACT GTT TTT AGA GAA GAT TGG
Leu Ala Ala Lys Asn His Ile Ser Leu Thr Val Phe Arg Glu Asp Trp

                                360
    *     *     *     *     *     *     *     *     *
CTA GAG AAT CTA ACG CTA GAA GCA ACA CTT CGA ATT CAT TTA AAA GTA
Leu Glu Asn Leu Thr Leu Glu Ala Thr Leu Arg Ile His Leu Lys Val
```

Fig. 1A

```
    390                                                 420
*     *       *       *       *       *       *       *       *       *
GAT AGC GGT ATG GGG CGT CTC GGT ATT CGT ACG ACT GAA GAA GCA CGG
Asp Ser Gly Met Gly Arg Leu Gly Ile Arg Thr Thr Glu Glu Ala Arg

                        450                                             480
  *       *       *     *       *       *       *       *       *     *
CGA ATT GAA GCA ACC AGT ACT AAT GAT CAC CAA TTA CAA CTG GAA GGT
Arg Ile Glu Ala Thr Ser Thr Asn Asp His Gln Leu Gln Leu Glu Gly

                                        510
     *       *       *       *       *       *       *       *       *
ATT TAC ACG CAT TTT GCA ACA GCC GAC CAG CTA GAA ACT AGT TAT TTT
Ile Tyr Thr His Phe Ala Thr Ala Asp Gln Leu Glu Thr Ser Tyr Phe

              540                                                   570
  *       *       *       *       *       *       *       *       *       *
GAA CAA CAA TTA GCT AAG TTC CAA ACG ATT TTA ACG AGT TTA AAA AAA
Glu Gln Gln Leu Ala Lys Phe Gln Thr Ile Leu Thr Ser Leu Lys Lys

                                600
    *       *       *       *       *       *       *       *       *
CGA CCA ACT TAT GTT CAT ACA GCC AAT TCA GCT GCT TCA TTG TTA CAG
Arg Pro Thr Tyr Val His Thr Ala Asn Ser Ala Ala Ser Leu Leu Gln

    630                                                 660
*     *       *       *       *       *       *       *       *       *
CCA CAA ATC GGG TTT GAT GCG ATT CGC TTT GGT ATT TCG ATG TAT GGA
Pro Gln Ile Gly Phe Asp Ala Ile Arg Phe Gly Ile Ser Met Tyr Gly

                        690                                             720
  *       *       *     *       *       *       *       *       *     *
TTA ACT CCC TCC ACA GAA ATC AAA ACT AGC TTG CCG TTT GAG CTT AAA
Leu Thr Pro Ser Thr Glu Ile Lys Thr Ser Leu Pro Phe Glu Leu Lys

                                        750
     *       *       *       *       *       *       *       *       *
CCT GCA CTT GCA CTC TAT ACC GAG ATG GTT CAT GTG AAA GAA CTT GCA
Pro Ala Leu Ala Leu Tyr Thr Glu Met Val His Val Lys Glu Leu Ala
```

Fig. 1B

```
            780                                                 810
 *      *     *      *      *      *      *      *      *      *
CCA GGC GAT AGC GTT AGC TAC GGA GCA ACT TAT ACA GCA ACA GAG CGA
Pro Gly Asp Ser Val Ser Tyr Gly Ala Thr Tyr Thr Ala Thr Glu Arg

                              840
    *     *      *      *     *      *      *     *      *
GAA TGG GTT GCG ACA TTA CCA ATT GGC TAT GCG GAT GGA TTG ATT CGT
Glu Trp Val Ala Thr Leu Pro Ile Gly Tyr Ala Asp Gly Leu Ile Arg

    870                                          900
*     *      *      *      *      *      *      *      *      *
CAT TAC AGT GGT TTC CAT GTT TTA GTA GAC GGT GAA CCA GCT CCA ATC
His Tyr Ser Gly Phe His Val Leu Val Asp Gly Glu Pro Ala Pro Ile

                       930                                          960
  *      *      *      *      *      *      *      *      *      *
ATT GGT CGA GTT TGT ATG GAT CAA ACC ATC ATA AAA CTA CCA CGT GAA
Ile Gly Arg Val Cys Met Asp Gln Thr Ile Ile Lys Leu Pro Arg Glu

                                      990
     *      *      *      *      *      *      *      *      *
TTT CAA ACT GGT TCA AAA GTA ACG ATA ATT GGC AAA GAT CAT GGT AAC
Phe Gln Thr Gly Ser Lys Val Thr Ile Ile Gly Lys Asp His Gly Asn

           1020                                                1050
 *      *      *      *      *      *      *      *      *      *
ACG GTA ACA GCA GAT GAT GCC GCT CAA TAT TTA GAT ACA ATT AAT TAT
Thr Val Thr Ala Asp Asp Ala Ala Gln Tyr Leu Asp Thr Ile Asn Tyr

                              1080
    *     *      *      *     *      *      *     *      *
GAG GTA ACT TGT TTG TTA AAT GAG CGC ATA CCT AGA AAA TAC ATC CAT
Glu Val Thr Cys Leu Leu Asn Glu Arg Ile Pro Arg Lys Tyr Ile His

*
TAG
 *
```

Fig. 1C

```
LMDAL      1  MVTGWHRPTWIEIDRAAIRENLKNEQNKLPES  32
BSTDAL     1  MNDFHRDTWAEVDLDAIYDNVENLRRLLPDD  31
BSUBDAL    1  MSTKPFYRDTWAEIDLSAIKENVSNMKKHIGEH  33

LMDAL     33  VDLWAVVKANAYGHGIIEVARTAKEAGAKGFCV  65
BSTDAL    32  THIMAVVKANAYGHGDVQVARTALERGPPP.AV  63
BSUBDAL   34  VHLMAVFKANAYGHGDAETAKAALDAGASCLAM  66

LMDAL     66  AILDEALALREAGFQDDFILVLGATRKEDANLA  98
BSTDAL    64  AFLDEALALREKGIEAP.ILVLGASRPADAALA  95
BSUBDAL   67  AILDEAISLRKKGLKAP.ILVLGAVPPEYVAIA  98

LMDAL     99  AKNHISLTVFREDWLENL.TL.EA...TLRI..  124
BSTDAL    96  AQQRIALTVFRSDWLEEASALYSG...PFPIHF  125
BSUBDAL   99  AEYDVTLTGYSVEWLQEA.AR.HTKKGSL..HF  127

LMDAL    125  HLKVDSGMGRLGIRTIEEARRIEATSTNDHQLQ  157
BSTDAL   126  HLKMDTGMGRLGVKDEEETKRIVALIERHPHFV  158
BSUBDAL  128  HLKVDTGMNRLGVKTEEEVQNVMAILDRNPRLK  160

LMDAL    158  LEGIYTHFATADQLETSYFEQQLAKFQTILTSL  190
BSTDAL   159  LEGLYTHFATADEVNTDYFSYQYTRFLHMLEWL  191
BSUBDAL  161  CKGVFTHFATADEKERGYFLMQFERFKELIAPL  193

LMDAL    191  KKRPTYVHTANSAASL.LQPQIGFDAIRFGISM  222
BSTDAL   192  PSRPPLVHCANSAASLR.FPDRTFNMVRFGIAM  223
BSUBDAL  194  PLKNLMVHCANSAAGLRLKKGF.FNAVRFGIGM  225

LMDAL    223  YGLTPSTEIKTSLPFELKPALALYTEMVHVKEL  255
BSTDAL   224  YGLAPSPGIKPLLPYPLKEAFSLHSRLVHVKKL  256
BSUBDAL  226  YGLRPSADMSDEIPFQLRPAFTLHSTLSHVKLI  258

LMDAL    256  APGDSVSYGATYTATEREWVATLPIGYADGLIR  288
BSTDAL   257  QPGEKVSYGATYTAQTEEWIGTIPIGYADG.VR  288
BSUBDAL  259  RKGESVSYGAEYTAEKDTWIGTVPVGYADGWLR  291
```

Fig. 2A

```
LMDAL     289 HYSGFHVLVDGEPAPIIGRVCMDQTIIKLPREF 321
BSTDAL    289 RLQHFHVLVDGQKAPIVGRICMDQCMIRLPGPL 321
BSUBDAL   292 KLKGTDILVKGKRLKIAGRICMDQFMVELDQEY 324

LMDAL     322 QTGSKVTIIGKDHGNTVTADDAAQYLDTINYEV 354
BSTDAL    322 PVGTKVTLIGRQGDEVISIDDVARHLETINYEV 354
BSUBDAL   325 PPGTKVTLIGRQGDEYISMDEIAGRLETINYEV 357

LMDAL     355 TCLLNERIPRKYIH                     368
BSTDAL    355 PCTISYRVPRIFFRHKRIMEVRNAIGRGESSA 386
BSUBDAL   358 ACTISSRVPRMFLENGSIMEVRNPLLQVNISN 389
```

Fig.-2B

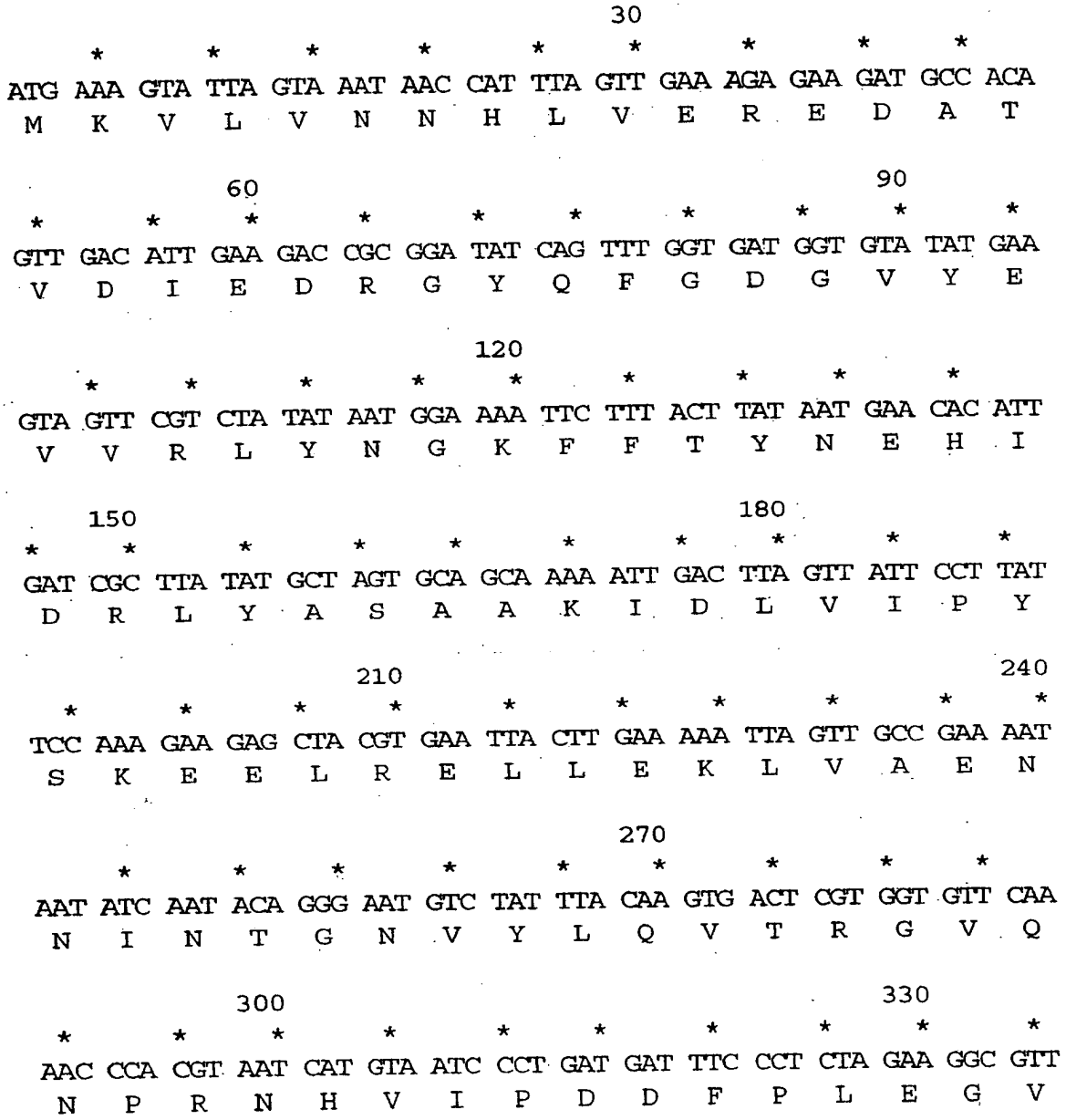
30
ATG AAA GTA TTA GTA AAT AAC CAT TTA GTT GAA AGA GAA GAT GCC ACA
M K V L V N N H L V E R E D A T
60
90
GTT GAC ATT GAA GAC CGC GGA TAT CAG TTT GGT GAT GGT GTA TAT GAA
V D I E D R G Y Q F G D G V Y E
120
GTA GTT CGT CTA TAT AAT GGA AAA TTC TTT ACT TAT AAT GAA CAC ATT
V V R L Y N G K F F T Y N E H I
150
180
GAT CGC TTA TAT GCT AGT GCA GCA AAA ATT GAC TTA GTT ATT CCT TAT
D R L Y A S A A K I D L V I P Y
210
240
TCC AAA GAA GAG CTA CGT GAA TTA CTT GAA AAA TTA GTT GCC GAA AAT
S K E E L R E L L E K L V A E N
270
AAT ATC AAT ACA GGG AAT GTC TAT TTA CAA GTG ACT CGT GGT GTT CAA
N I N T G N V Y L Q V T R G V Q
300
330
AAC CCA CGT AAT CAT GTA ATC CCT GAT GAT TTC CCT CTA GAA GGC GTT
N P R N H V I P D D F P L E G V

Fig. 3A

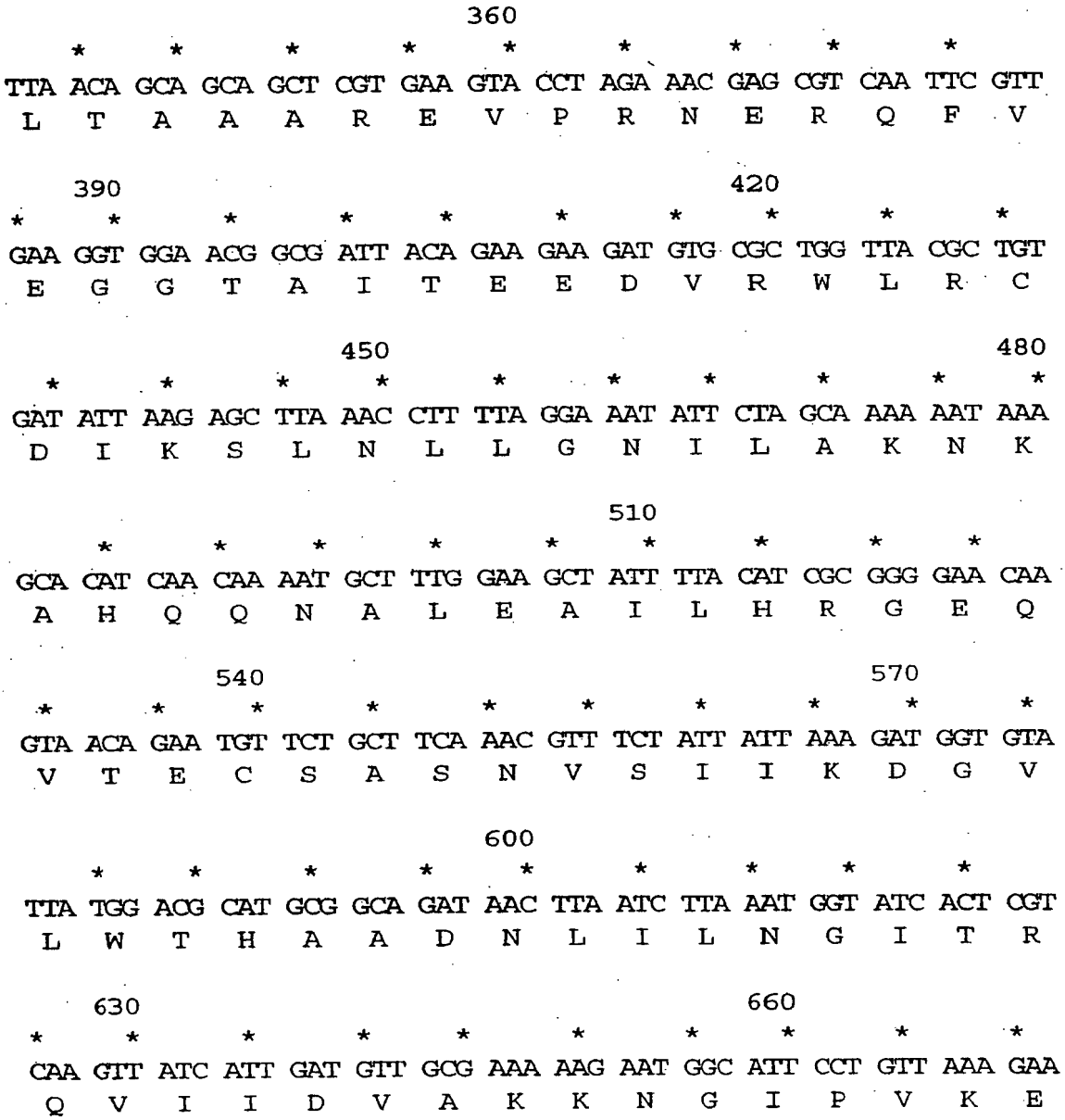
360
TTA ACA GCA GCA GCT CGT GAA GTA CCT AGA AAC GAG CGT CAA TTC GTT
L T A A A R E V P R N E R Q F V
390
420
GAA GGT GGA ACG GCG ATT ACA GAA GAA GAT GTG CGC TGG TTA CGC TGT
E G G T A I T E E D V R W L R C
450
480
GAT ATT AAG AGC TTA AAC CTT TTA GGA AAT ATT CTA GCA AAA AAT AAA
D I K S L N L L G N I L A K N K
510
GCA CAT CAA CAA AAT GCT TTG GAA GCT ATT TTA CAT CGC GGG GAA CAA
A H Q Q N A L E A I L H R G E Q
540
570
GTA ACA GAA TGT TCT GCT TCA AAC GTT TCT ATT ATT AAA GAT GGT GTA
V T E C S A S N V S I I K D G V
600
TTA TGG ACG CAT GCG GCA GAT AAC TTA ATC TTA AAT GGT ATC ACT CGT
L W T H A A D N L I L N G I T R
630
660
CAA GTT ATC ATT GAT GTT GCG AAA AAG AAT GGC ATT CCT GTT AAA GAA
Q V I I D V A K K N G I P V K E

Fig. 3B

```
                          690                                                 720
  *       *       *       *       *       *       *       *       *       *
GCG GAT TTC ACT TTA ACA GAC CTT CGT GAA GCG GAT GAA GTG TTC ATT
 A   D   F   T   L   T   D   L   R   E   A   D   E   V   F   I

                                  750
    *       *       *       *       *       *       *       *       *
TCA AGT ACA ACT ATT GAA ATT ACA CCT ATT ACG CAT ATT GAC GGA GTT
 S   S   T   T   I   E   I   T   P   I   T   H   I   D   G   V

            780                                                 810
  *       *       *       *       *       *       *       *       *       *
CAA GTA GCT GAC GGA AAA CGT GGA CCA ATT ACA GCG CAA CTT CAT CAA
 Q   V   A   D   G   K   R   G   P   I   T   A   Q   L   H   Q

                              840
    *       *       *       *       *       *       *       *       *
TAT TTT GTA GAA GAA ATC ACT CGT GCA TGT GGC GAA TTA GAG TTT GCA
 Y   F   V   E   E   I   T   R   A   C   G   E   L   E   F   A

    870
*       *
AAA TAA
 K   *
```

Fig. 3C

```
LMDAT       1 M.KVLVNNHLVEREDATVDIEDRGYQFGDGVYE   32
SHAEDAT     1 MTKVFINGEFIDQNEAKVSYEDRGYVFGDGIYE   33
BSPHDAT     1 MAYSLWNDQIVEEGSITISPEDRGYQFGDGIYE   33
BSPDAT      1 MGYTLWNDQIVKDEEVKIDKEDRGYQFGDGVYE   33

LMDAT      33 VVRLYNGKFFTYNEHIDRLYASAAKIDLVIPYS   65
SHAEDAT    34 YIRAYDGKLFTVTEHFERFIRSASEIQLDLGYT   66
BSPHDAT    34 VIKVYNGHMFTAQEHIDRFYASAEKIRLVIPYT   66
BSPDAT     34 VVKVYNGEMFTVNEHIDRLYASAEKIRITIPYT   66

LMDAT      66 KEELRELLEKLVAENNIINTGNVYLQVTRGVQNP   98
SHAEDAT    67 VEELIDVVRELLKVNNIQNGGIYIQATRGV.AP   98
BSPHDAT    67 KDVLHKLLHDLIEKNNLNTGHVYFQITRGT.TS   98
BSPDAT     67 KDKFHQLLHELVEKNELNTGHIYFQVTRGT.SP   98

LMDAT      99 RNHVIPDDFFPLEGVLTAAAREVPRNERQFVEGG 131
SHAEDAT    99 RNHSFPT.PEVKPVIMAFAKSYDRPYDDLENGI 130
BSPHDAT    99 RNHIFPD.ASVPAVLTGNVKTGERSIENFEKGV 130
BSPDAT     99 RAHQFPEN.TVKPVIIGYTKENPRPLENLEKGV 130

LMDAT     132 TAITEEDVRWLRCDIKSLNLLGNILAKNKAHQQ 164
SHAEDAT   131 NAATVEDIRWLRCDIKSLNLLGNVLAKEYAVKY 163
BSPHDAT   131 KATLVEDVRWLRCDIKSLNLLGAVLAKQEASEK 163
BSPDAT    131 KATFVEDIRWLRCDIKSLNLLGAVLAKQEAHEK 163

LMDAT     165 NALEAILHRGEQVTECSASNVSIIKDGVLWTHA 197
SHAEDAT   164 NAGEAIQHRGETVTEGASSNVYAIKDGAIYTHP 196
BSPHDAT   164 GCYEAILHRGDIITECSSANVYGIKDGKLYTHP 196
BSPDAT    164 GCYEAILHRNNTVTEGSSSNVFGIKDGILYTHP 196

LMDAT     198 ADNLILNGITRQVIIDVAKKNGIPVKEADFTLT 230
SHAEDAT   197 VNNYILNGITRKVIKWISEDEDIPFKEETFTVE 229
BSPHDAT   197 ANNYILNGITRQVILKCAAEINLPVIEEPMIKG 229
BSPDAT    197 ANNMILKGITRDVVIACANEINMPVKEIPFTTH 229
```

Fig. 4A

```
LMDAT     231 DLREADEVFISSTTIEITPITHIDGVQVADGKR 263
SHAEDAT   230 FLKNADEVIVSSTSAEVTPVVKIDGEQVGDGKV 262
BSPHDAT   230 DLLTMDEIIVSSVSSEVTPVIDVDGQQIGAGVP 262
BSPDAT    230 EALKMDELFVTSTTSEITPVIEIDGKLIRDGKV 262

LMDAT     264 GPITAQLHQYFVEEITRACGELEFAK 289
SHAEDAT   263 GPVTRQLQEGFNKYIESRSS 282
BSPHDAT   263 GEWTRKLQKAFEAKLPISINA 283
BSPDAT    263 GEWTRKLQKQFETKIPKPLHI 283
```

Fig. 4B

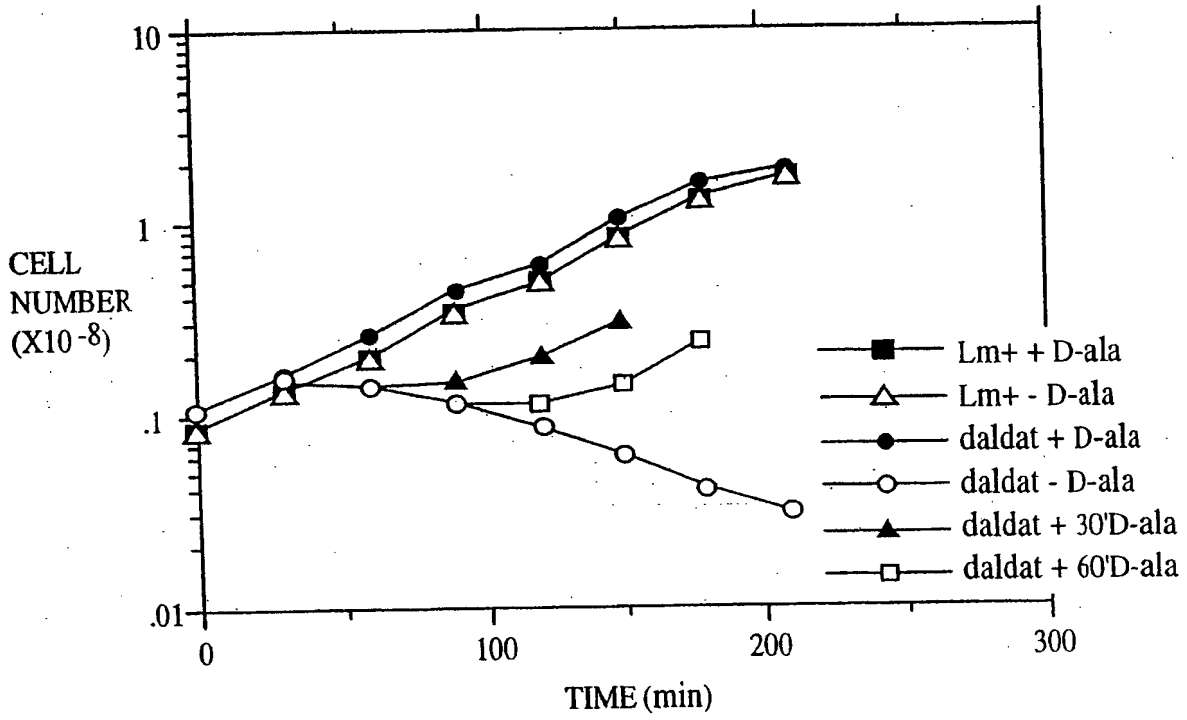
10
1
.1
.01
CELL
NUMBER
(X10 -8)
0
100
200
300
TIME (min)
Lm+ + D-ala
Lm+ - D-ala
daldat + D-ala
daldat - D-ala
daldat + 30'D-ala
daldat + 60'D-ala

Fig. 5

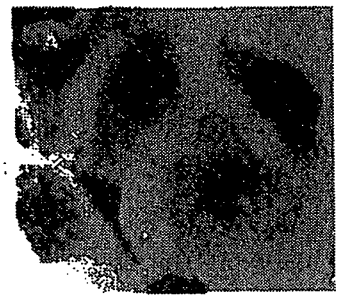

FIG.6A

FIG.6B

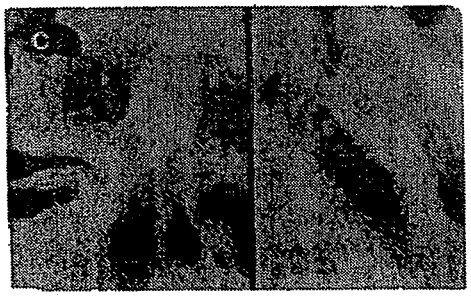

FIG.6C

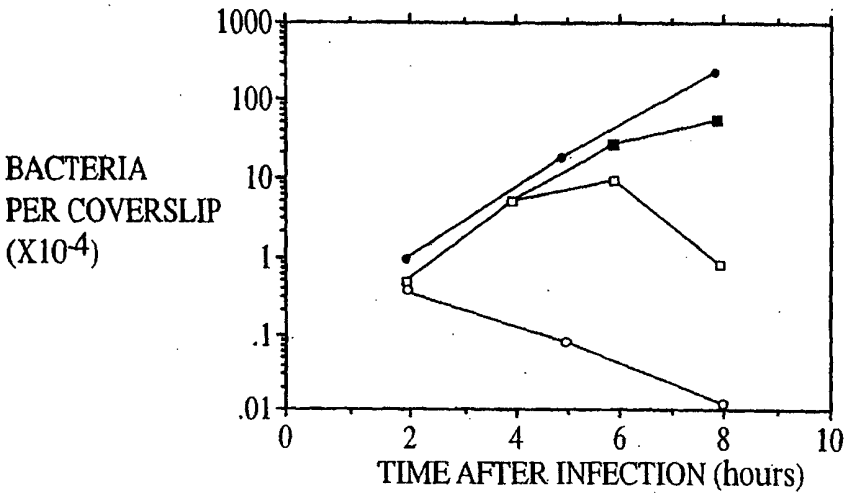

Fig. 7A

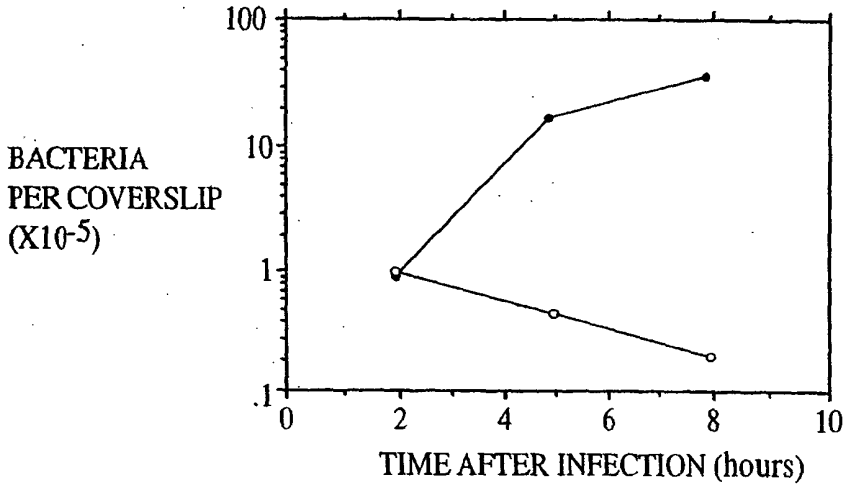

Fig. 7B

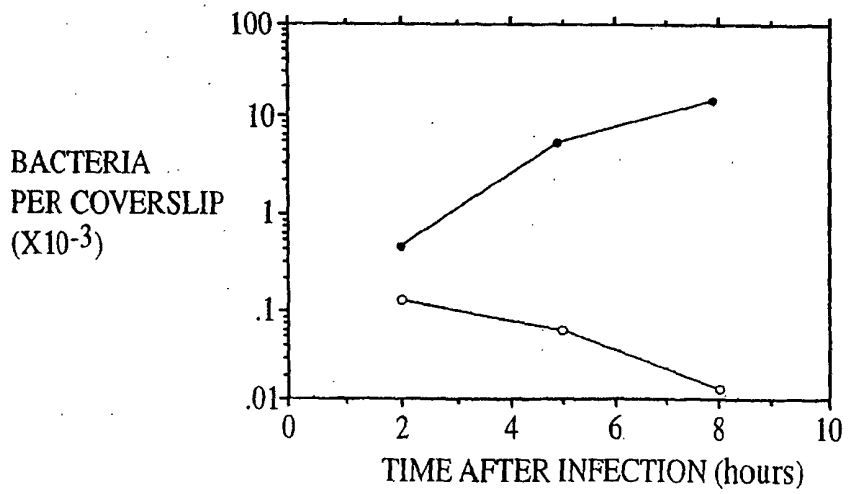

Fig. 7C

FIG.8A FIG.8B FIG.8C FIG.8D FIG.8E

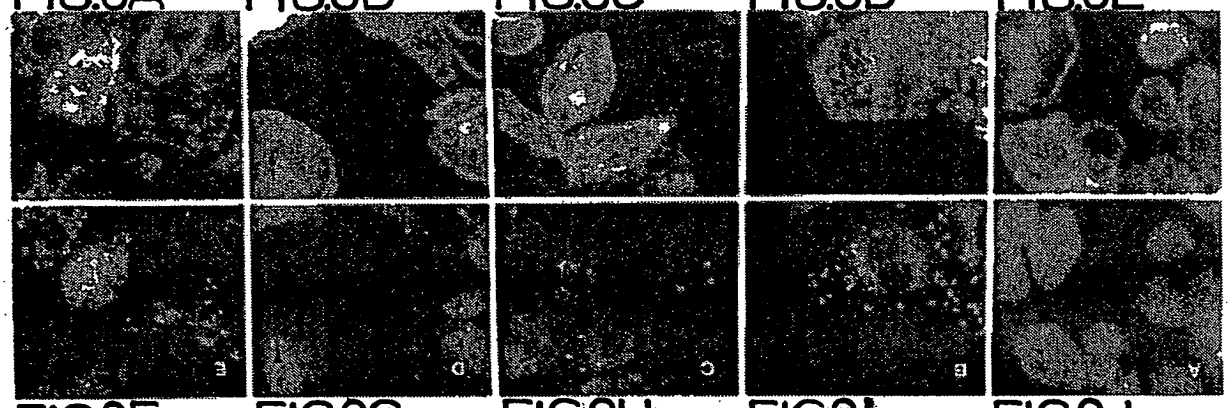

FIG.8F FIG.8G FIG.8H FIG.8I FIG.8J

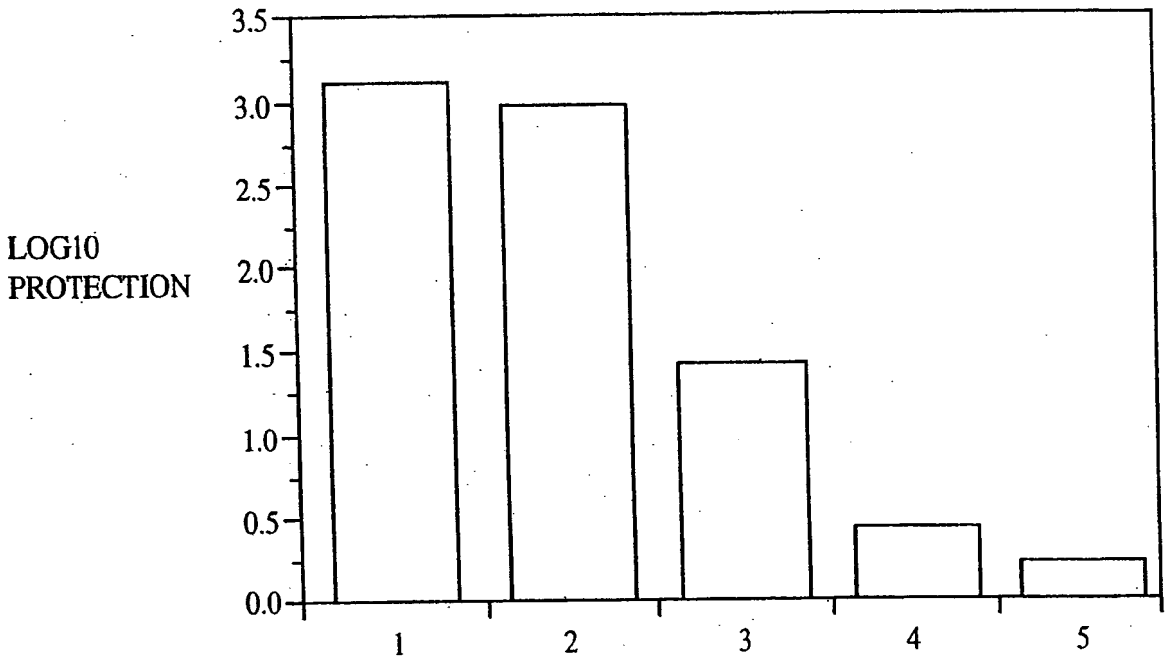

Fig. 9

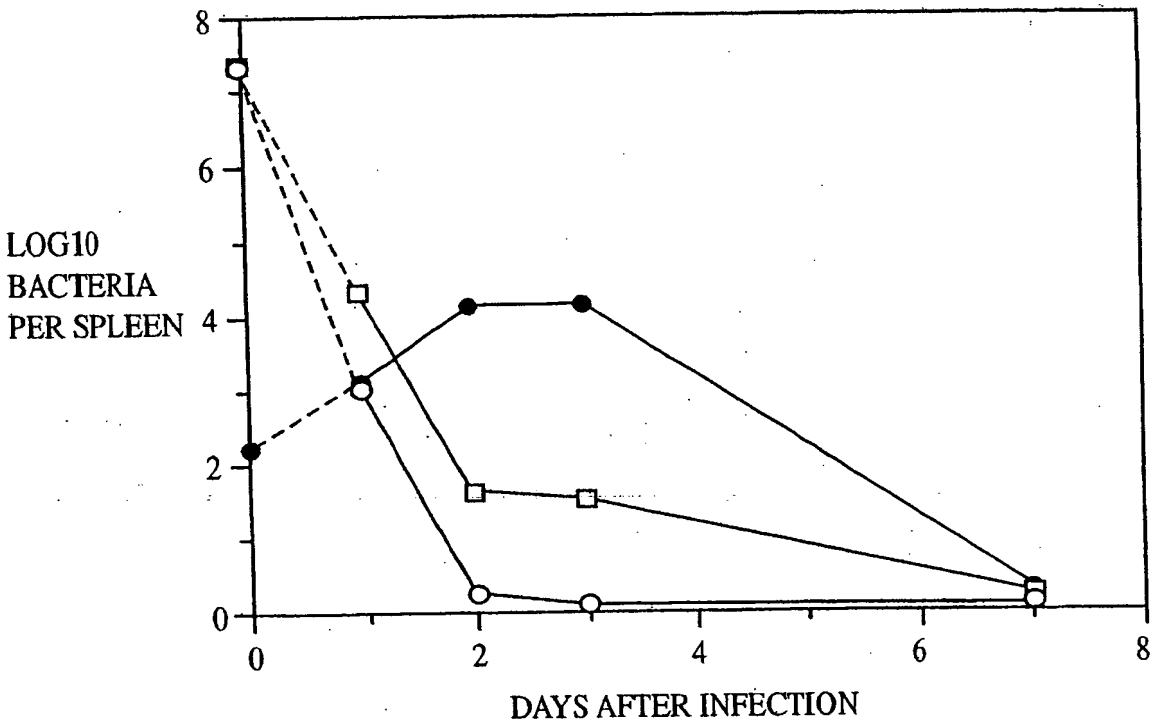
LOG10
BACTERIA
PER SPLEEN
8
6
4
2
0
0
2
4
6
8
DAYS AFTER INFECTION

Fig. 10

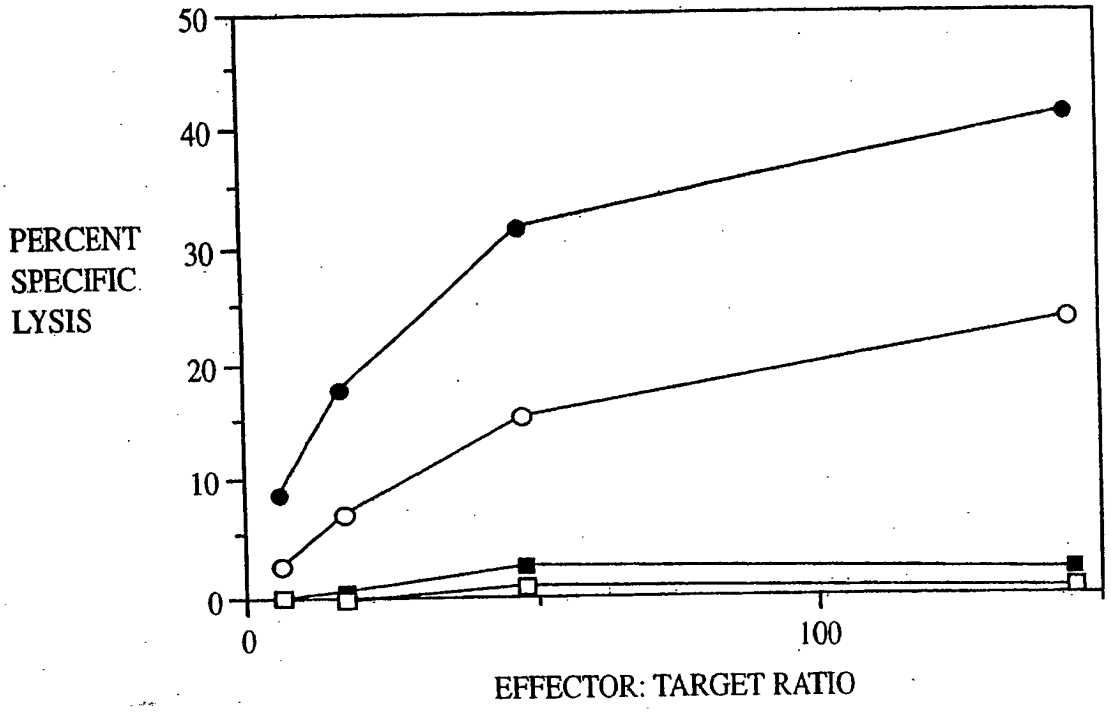

Fig. 11A

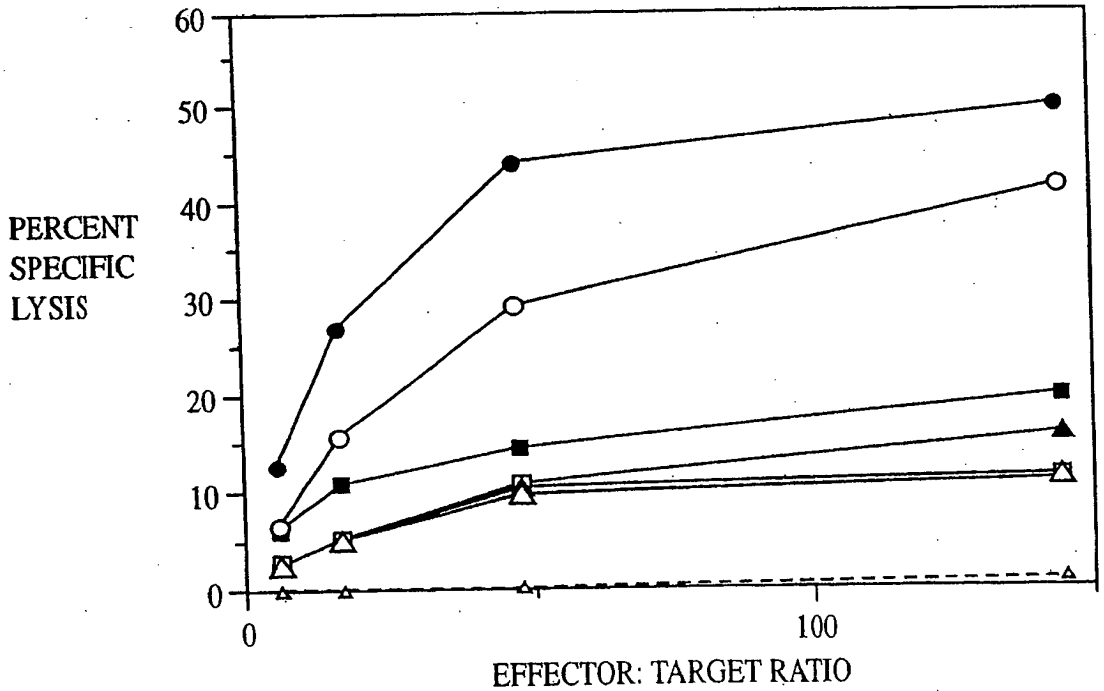

Fig. 11B